an amino acid specific protease (*e.g.*, Lys-C, trypsin), and then determine the mass of the resulting peptide fragments using mass spectroscopy. Determination of peptide mass can then be used to identify the protein as SGT4, or a variant thereof, using a database of the predicted masses of protein proteolysis products and analysis software such as Protein Prospector, which is publicly available on the internet.

IN THE CLAIMS:

A marked-up version of the claims showing the amendments is attached hereto as Exhibit A. Matter that has been deleted from claims 1, 3, 4, and 5, is indicated by brackets and matter that has been added is indicated by underlining.

Please amend the claims as follows:

1. (Twice Amended) An isolated nucleic acid molecule comprising at least 50 contiguous bases of SEQ ID NO:1 or 3, or the complement thereof.

3. (Twice Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that comprises at least 50 contiguous bases and that hybridizes under stringent conditions to a second nucleic acid molecule consisting of: (a) the nucleic acid sequence of SEQ ID NO:1 or 3; or (b) a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO:2 or 4, or the complement thereof, wherein the stringent conditions comprise hybridization in 6xSSC, 50mM Tris HCl (pH 7.5), 1mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500µg/ml denatured salmon sperm DNA at 65°C, and washing in 0.1x SSC at 50°C.

4. (Twice Amended) A recombinant vector comprising the nucleic acid molecule of Claim 1, 2, or 3.

5. (Twice Amended) An expression vector comprising the nucleic acid molecule of Claim 1, 2, or 3 operatively associated with a regulatory nucleic acid that controls the expression of the nucleic acid molecule in a host cell.

REMARKS

Claims 1-6, 8, and 21 are pending after entry of this amendment. Claims 1, 3, 4, and 5 have been amended to more particularly point out and distinctly claim that which